

when a new primer data is added to the database (not shown in the figures). Fig. 16 is a desktop image diagram showing a selection of the primer data of the primer set as described above. (In the screen shown in Fig. 16, the user can select the respective primer data.) The forward primer used in Fig. 16 is named "41f", has a base sequence of "gctcagattgaactcggcg" of SEQ ID NO. 3, and has an allowance limit for mismatch of 4%. Similarly, the reverse primer is named "1066r", has a base sequence of "acatttcacaacacgagctg" of SEQ ID NO:4, and has an allowance limit for mismatch of 4%. The primer data thus selected are utilized by the amplified sequence recognizing portion 31 when the base sequence in the region to be amplified by using the primer set is extracted from the pre-amplification base sequence of the known gene.--

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Please delete the original Sequence Listing.

Page 33 (Abstract), after the last line, beginning on a new page, please insert the attached substitute Sequence Listing.

REMARKS

Claims 1-15 are pending in the present application.

Applicants have now submitted a substitute Sequence Listing and a corresponding computer-readable Sequence Listing. The sequence information recorded in the corresponding computer-readable Sequence Listing is identical to the paper copy of the substitute Sequence Listing. Support for all of the sequences listed in the substitute Sequence Listing is found in the present application as originally filed. No new matter is believed to have been introduced by the submission of the substitute Sequence Listing and the corresponding computer-readable Sequence Listing.

Applicants submit that the present application is ready for examination on the merits.

Early notice to this effect is earnestly solicited.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
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IN THE SPECIFICATION

Page 19, line 24 to page 20, line 12, please replace the paragraph with the following paragraph:

--At first, the primer data, which includes information on the base sequences, the names, and the allowance limits for mismatch of predetermined forward primer and reverse primer, are input and registered in the primer database. The folder having the names of both primers, in which the post-amplification base sequence is saved, is automatically formed when a new primer data is added to the database (not shown in the figures). Fig. 16 is a desktop image diagram showing a selection of the primer data of the primer set as described above. (In the screen shown in Fig. 16, the user can select the respective primer data.) The forward primer used in Fig. 16 is named "41f", has a base sequence of "gctcagattgaactcggcg" of SEQ ID NO. 3, and has an allowance limit for mismatch of 4%. Similarly, the reverse primer is named "1066r", has a base sequence of "acatttcacaacacgagctg" of SEQ ID NO:4, and has an allowance limit for mismatch of 4%. The primer data thus selected are utilized by the amplified sequence recognizing portion 31 when the base sequence in the region to be amplified by using the primer set is extracted from the pre-amplification base sequence of the known gene.--



22850